

0590  
1012

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/935,390A

DATE: 11/19/2001

TIME: 15:40:33

Input Set : N:\Crf3\RULE60\09935390A.txt

Output Set: N:\CRF3\11192001\I935390A.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Escobedo, Jaime

6 Quianjin, Hu

7 Garcia, Pablo

8 Williams, Lewis T.

9 Kothakota, Srinivas

C--> 11 (ii) TITLE OF INVENTION: Secreted Human Proteins

13 (iii) NUMBER OF SEQUENCES: 38

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Chiron Corporation

17 (B) STREET: 4560 Horton Street

18 (C) CITY: Emeryville

19 (D) STATE: CA

20 (E) COUNTRY: USA

21 (F) ZIP: 94608-2916

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Diskette

25 (B) COMPUTER: IBM Compatible

26 (C) OPERATING SYSTEM: DOS

27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/935,390A

C--> 31 (B) FILING DATE: 22-Aug-2001

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/988,671

36 (B) FILING DATE: 1997-12-11

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Jane E. R. Potter

40 (B) REGISTRATION NUMBER: 33,332

41 (C) REFERENCE/DOCKET NUMBER: 1369.002

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (510) 923-2718

45 (B) TELEFAX: (510) 655-3542

46 (C) TELEX:

49 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 2063 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

55 (ix) FEATURE:

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 GAATTTCGGCA CGAGGCCTCA GTCTTCCAGG GCGGCGGTGG GTGTCCGCTT CTCTCTGCTC 60

59 TTCGACTGCA CCGCACTCGC GCGTGACCCT GACTCCCCCT AGTCAGCTCA GCGGTGCTGC 120

60 CATGGCGTGG CGGCGGCGCG AAGCCGGCGT CGGGGCTCGC GCGGTGTTGG CTCTGGCGTT 180

ENTERED

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61	GCTCGCCCTG	GCCCTGTGCG	TGCCCCGGGGC	CCGGGGCCGG	GCTCTCGAGT	GGTTCTCGGC	240
62	CGTGGTAAAC	ATCGAGTACG	TGGACCCGCA	GACCAACCTG	ACGGTGTGGA	GCGTCTCGGA	300
63	GAGTGGCCGC	TTCGGCGACA	GCTCGCCCAA	GGAGGGCGCG	CATGGCCTGG	TGGGCGTCCC	360
64	GTGGGCGCCC	GGCGGAGACC	TCGAGGGCTG	CGCGCCCGAC	ACGCGCTTCT	TCGTGCCCCG	420
65	GCCCCGGCGC	CGAGGGGCGG	CGCCCTGGGT	CGCCCTGGTG	GCTCGTGGGG	GCTGCACCTT	480
66	CAAGGACAAG	GTGCTGGTGG	CGGCGCGGAG	GAACGCCTCG	GCCGTCGTCC	TCTACAATGA	540
67	GGAGCGCTAC	GGGAACATCA	CCTTGCCCAT	GTCTCACGCG	GGAACAGGAA	ATATAGTGGT	600
68	CATTATGATT	AGCTATCCAA	AAGGAAGAGA	AATTTTGGAG	CTGGTGCAAA	AAGGAATTCC	660
69	AGTAACGATG	ACCATAGGGG	TTGGCACCCG	GCATGTACAG	GAGTTCATCA	GCGGTCAGTC	720
70	TGTGGTGTTT	GTGGCCATTG	CCTTCATCAC	CATGATGATT	ATCTCGTTAG	CCTGGCTAAT	780
71	ATTTTACTAT	ATACAGCGTT	TCCTATATAC	TGGCTCTCAG	ATTGGAAGTC	AGAGCCATAG	840
72	AAAAGAAACT	AAGAAAGTTA	TTGGCCAGCT	TCTACTTCAT	ACTGTAAAGC	ATGGAGAAAA	900
73	GGGAATTGAT	GTTGATGCTG	AAAATTGTGC	AGTGTGTATT	GAAAATTTCA	AAGTAAAGGA	960
74	TATTATTAGA	ATTCTGCCAT	GCAAGCATAT	TTTTCATAGA	ATATGCATTG	ACCCATGGCT	1020
75	TTTGGATCAC	CGAACATGTC	CAATGTGTAA	ACTTGATGTC	ATCAAAGCCC	TAGGATATTG	1080
76	GGGAGAGCCT	GGGGATGTAC	AGGAGATGCC	TGCTCCAGAA	TCTCCTCCTG	GAAGGGATCC	1140
77	AGCTGCAAAT	TTGAGTCTAG	CTTTACCAGA	TGATGACGGA	AGTGATGACA	GCAGTCCACC	1200
78	ATCAGCCTCC	CCTGCTGAAT	CTGAGCCACA	GTGTGATCCC	AGCTTTAAAG	GAGATGCAGG	1260
79	AGAAAATACG	GCATTGCTAG	AAGCCGGCAG	GAGTGACTCT	CGGCATGGAG	GACCCATCTC	1320
80	CTAGCACACG	TGCCCCTGA	AGTGGCACCA	ACAGAAGTTT	GGCTTGAAC	AAAGGACATT	1380
81	TTATTTTTTT	TACTTTAGCA	CATAATTTGT	ATATTTGAAA	ATAATGTATA	TTATTTTACC	1440
82	TATTAGATTC	TGATTTGATA	TACAAAGGAC	TAAGATATTT	TCTTCTTGAA	GAGACTTTTC	1500
83	GATTAGTCCT	CATATATTTA	TCTACTAAAA	TAGAGTGTTT	ACCATGAACA	GTGTGTTGCT	1560
84	TCAGACTATT	ACAAAGACAA	CTGGGGCAGG	TACTCTAATA	TAAAGGACAG	GTGGTGTTTC	1620
85	TAAATAATTG	GCTGCTATGG	TTCTGTAAAA	ACCAGTTAAT	TCTATTTTTC	AAGGTTTTTG	1680
86	GCAAAGCACA	TCAATGTTAG	ACTAGTTGAA	GTGGAATTGT	ATAATTCAAT	TCGATAATTG	1740
87	ATCTCATGGG	CTTTCCCTGG	AGGAAAGGTT	TTTTTTTGTT	TTTTTTTTTT	AAGAACTTGA	1800
88	AACTTGTAAG	CTGAGATGTC	TGTAGCTTTT	TTGCCCATCT	GTAGTGTATG	TGAAGATTTC	1860
89	AAAACCTGAG	AGCACTTTTT	CTTTGTTTAG	AATTATGAGA	AAGGCACTAG	ATGACTTTAG	1920
90	GATTTGCATT	TTTCCCTTTA	TTGCCTCATT	TCTTGTGACG	CCTTGTTGGG	GAGGGAAATC	1980
91	TGTTTATTTT	TTCCTACAAA	TAAAAAGCTA	AGATTCTATA	TCGCAAAAAA	AAAAAAAAAA	2040
92	AAAAAAAAAA	TTCCTGCGGC	CGC				2063
94	(2) INFORMATION FOR SEQ ID NO: 2:						
95	(i) SEQUENCE CHARACTERISTICS:						
96	(A) LENGTH: 1328 base pairs						
97	(B) TYPE: nucleic acid						
98	(C) STRANDEDNESS: single						
99	(D) TOPOLOGY: linear						
100	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:						
102	GAATTCGGCA	CGAGGTAGGC	AAGGGATAAA	AAGGCACCTA	AGGCCCTTTT	GCAATAAGAA	60
103	GCCAGATGGA	TAAAGGAAGT	GCTGGTCACC	CTGGAGGTGT	ACTGGTTTGG	GGAAGGTCCC	120
104	CGGCCCCCAC	AGCCCTCTGG	GGAGCCTCAC	CCTGGCTCTC	CCCACTCACC	TCAGCCCTCA	180
105	GGCAGCCCCCT	CCACAGGGCC	CCTCTCCTGC	CTGGACAGCT	CTGCTGGTCT	CCCCGTCCCC	240
106	TGGAGAAGAA	CAAGGCCATG	GGTCGGCCCC	TGCTGCTGCC	CCTGCTGCTC	CTGCTGCAGC	300
107	CGCCAGCATT	TCTGCAGCCT	GGTGGCTCCA	CAGGATCTGG	TCCAAGCTAC	CTTTATGGGG	360
108	TCACTCAACC	AAAACACCTC	TCAGCCTCCA	TGGGTGGCTC	TGTGGAAATC	CCCTTCTCCT	420
109	TCTATTACCC	CTGGGAGTTA	GCCATAGTTC	CCAACGTGAG	AATATCCTGG	AGACGGGGCC	480
110	ACTTCCACGG	GCAGTCCTTC	TACAGCACAA	GGCCGCCTTC	CATTCACAAG	GATTATGTGA	540
111	ACCGGCTCTT	TCTGAACTGG	ACAGAGGGTC	AGGAGAGCGG	CTTCCTCAGG	ATCTCAAACC	600

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112  TGCGGAAGGA  GGACCAGTCT  GTGTATTTCT  GCCGAGTCGA  GCTGGACACC  CGGAGATCAG  660
113  GGAGGCAGCA  GTTGCAGTCC  ATCAAGGGGA  CCAAACCTCAC  CATCACCCAG  GCTGTCACAA  720
114  CCACCACCAC  CTGGAGGCC  AGCAGCACAA  CCACCATAGC  CGGCCTCAGG  GTCACAGAAA  780
115  GCAAAGGGCA  CTCAGAATCA  TGGCACCTAA  GTCTGGACAC  TGCCATCAGG  GTTGCATTGG  840
116  CTGTCGCTGT  GCTCAAACT  GTCATTTTGG  GACTGCTGTG  CCTCCTCCTC  CTGTGGTGGA  900
117  GGAGAAGGAA  AGGTAGCAGG  GCGCCAAGCA  GTGACTTCTG  ACCAACAGAG  TGTGGGGAGA  960
118  AGGGATGTGT  ATTAGCCCCG  GAGGACGTGA  TGTGAGACCC  GCTTGTGAGT  CCTCCACACT  1020
119  CGTTCCCAT  TGGCAAGATA  CATGGAGAGC  ACCCTGAGGA  CCTTTAAAAG  GCAAAGCCGC  1080
120  AAGGCAGAAG  GAGGCTGGGT  CCCTGAATCA  CCGACTGGAG  GAGAGTTACC  TACAAGAGCC  1140
121  TTCATCCAGG  AGCATCCACA  CTGCAATGAT  ATAGGAATGA  GGTCTGAAC  CCACTGAATT  1200
122  AAACCACTGG  CATTTGGGG  CTGTTTATTA  TAGCAGTGCA  AAGAGTTCCT  TTATCCTCCC  1260
123  CAAGGATGGA  AAAATACAAT  TTATTTTGCT  TACCATAAAA  AAAAAAAAAA  AAAAATTCCT  1320
124  GCGGCCGC  1328
126  (2) INFORMATION FOR SEQ ID NO: 3:
127      (i) SEQUENCE CHARACTERISTICS:
128          (A) LENGTH: 1689 base pairs
129          (B) TYPE: nucleic acid
130          (C) STRANDEDNESS: single
131          (D) TOPOLOGY: linear
132      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
134  GAATTCGGCA  CGAGGGCAAG  ATTCGATACA  AAACCAATGA  ACCTGTGTGG  GAGGAAACT  60
135  TCACTTTCTT  CATTCACAAT  CCCAAGCGCC  AGGACCTTGA  AGTTGAGGTC  AGAGACGAGC  120
136  AGCACCAGTG  TTCCCTGGGG  AACCTGAAGG  TCCCCCTCAG  CCAGCTGCTC  ACCAGTGAGG  180
137  ACATGACTGT  GAGCCAGCGC  TTCCAGCTCA  GTAACCTCGG  TCCAAACAGC  ACCATCAAGA  240
138  TGAAGATTGC  CCTGCGGGTG  CTCCATCTCG  AAAAGCGAGA  AAGGCCTCCA  GACCACCAAC  300
139  ACTCAGCTCA  AGTCAAACGT  CCCTCTGTGT  CCAAAGAGGG  GAGGAAACA  TCCATCAAAT  360
140  CTCATATGTC  TGGGTCTCCA  GGCCCTGGTG  GCAGCAACAC  AGCTCCATCC  ACACCAGTCA  420
141  TTGGGGGCAG  TGATAAGCCT  GGTATGGAAG  AAAAGGCCCA  GCCCCCTGAG  GCCGGCCCTC  480
142  AGGGGCTGCA  CGACCTGGGC  AGAAGCTCCT  CCAGCCTCCT  GGCCTCCCA  GGCCACATCT  540
143  CAGTCAAGGA  GCCGACCCCC  AGCATCGCCT  CGGACATCTC  GCTGCCCATC  GCCACCCAGG  600
144  AGCTGCGGCA  AAGGCTGAGG  CAGCTGGAAA  ACGGGACGAC  CCTGGGACAG  TCTCCACTGG  660
145  GGCAGATCCA  GCTGACCATC  CGGCACAGCT  CGCAGAGAAA  CAAGCTTATC  GTGGTCGTGC  720
146  ATGCCTGCAG  AAACCTCATT  GCCTTCTCTG  AAGACGGCTC  TGACCCCTAT  GTCCGCATGT  780
147  ATTTATTACC  AGACAAGAGG  CGGTCAGGAA  GGAGGAAAC  ACACGTGTCA  AAGAAAACAT  840
148  TAAATCCAGT  GTTTGATCAA  AGCTTTGATT  TCAGTGTTTC  GTTACCAGAA  GTGCAGAGGA  900
149  GAACGCTCGA  CGTTGCCGTG  AAGAACAGTG  GCGGCTTCCT  GTCCAAAGAC  AAAGGGCTCC  960
150  TTGGCAAAGT  ATTGGTTGCT  CTGGCATCTG  AAGAACTTGC  CAAAGGCTGG  ACCCAGTGGT  1020
151  ATGACCTCAC  GGAAGATGGG  ACGAGGCCTC  AGGCGATGAC  ATAGCCGCAG  CAGGCAGGAG  1080
152  GCGTCCTCTT  CAGCGTAGCT  CTCCACCTCT  ACCCGGAACA  CACCCTCTCA  CAGACGTACC  1140
153  AATGTTATTT  TTATAATTTT  ATGGATTTAG  TTATACATAC  CTTAATAGTT  TTATAAAATT  1200
154  GTTGACATTT  CAGGCAAATT  TGGCCAATAT  TATCATTGAA  TTTTCTGTGT  TGGATTTCTT  1260
155  CTAGGATTTT  GCCAGTTCCT  ACAACGTGCA  GTAGGGCGGC  GGTAGCTCTT  GTGTCTGTGG  1320
156  ACTCTGCTCA  GCTGTGTCCG  TAGGAGTCGG  ATGTGTCTGT  GCTTTATTAT  GGCCTTGTTT  1380
157  ATATATCACT  GAGGTATACT  ATGCCATGTA  AATAGACTAT  TTTTATAAAT  CTTAACATGC  1440
158  TGGTTTAAAT  TCAGAAGGAA  ATAGATCAAG  GAAATATATA  TATTTTCTTC  TAAAACCTAT  1500
159  TAAATTCGTG  TGACAAATAA  TCATTTTCAT  CTTGGCAGCA  AAAAGTTCTC  AGTGACCTAT  1560
160  TTTGTGGTGT  TTCTTTTGA  AAAGAAAAGC  TGAAATATTA  TTAAATGCTA  GTATGTTTCT  1620
161  GCCCATTATG  AAAGATGAAA  TAAAGTATTC  AAAATATTAA  AAAAAAAAAA  AAAAATTCC  1680
162  TGCGGCCGC  1689

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Input Set : N:\Crf3\RULE60\09935390A.txt

Output Set: N:\CRF3\11192001\I935390A.raw

165 (2) INFORMATION FOR SEQ ID NO: 4:

166 (i) SEQUENCE CHARACTERISTICS:

167 (A) LENGTH: 1505 base pairs

168 (B) TYPE: nucleic acid

169 (C) STRANDEDNESS: single

170 (D) TOPOLOGY: linear

171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

173	GAATTCGGCA	CGAGGAGCAG	ATCTGCAAGA	GTTTCGTTTA	TGGAGGCTGC	TTGGGCAACA	60
174	AGAACAATA	CCTTCGGGAA	GAAGAGTGCA	TTCTAGCCTG	TCGGGGTGTC	CAAGGTGGGC	120
175	CTTTGAGAGG	CAGCTCTGGG	GCTCAGGCGA	CTTTCCCCCA	GGCCCCCTCC	ATGGAAAGGC	180
176	GCCATCCAGT	GTGCTCTGGC	ACCTGTCAGC	CCACCCAGTT	CCGCTGCAGC	AATGGCTGCT	240
177	GCATCGACAG	TTTCCTGGAG	TGTGACGACA	CCCCCAACTG	CCCCGACGCC	TCCGACGAGG	300
178	CTGCCTGTGA	AAAATACACG	AGTGGCTTTG	ACGAGCTCCA	GCGCATCCAT	TTCCCCAGCG	360
179	ACAAAGGGCA	CTGCGTGGAC	CTGCCAGACA	CAGGACTCTG	CAAGGAGAGC	ATCCCGCGCT	420
180	GGTACTACAA	CCCCTTCAGC	GAACACTGCG	CCCGCTTTAC	CTATGGTGGT	TGTTACGGCA	480
181	ACAAGAACAA	CTTTGAGGAA	GAGCAGCAGT	GCCTCGAGTC	TTGTGCGGGC	ATCTCCAAGA	540
182	AGGATGTGTT	TGGCCTGAGG	CGGGAAATCC	CCATTCCCAG	CACAGGCTCT	GTGGAGATGG	600
183	CTGTCGCAGT	GTTCTGGTC	ATCTGCATTG	TGGTGGTGGT	AGCCATCTTG	GGTTACTGCT	660
184	TCTTCAAGAA	CCAGAGAAAG	GACTTCCACG	GACACCACCA	CCACCCACCA	CCCACCCCTG	720
185	CCAGCTCCAC	TGTCTCCACT	ACCGAGGACA	CGGAGCACCT	GGTCTATAAC	CACACCACGC	780
186	GGCCCCCTCTG	AGCCTGGGTC	TCACCGGCTC	TCACCTGGCC	CTGCTTCCTG	CTTGCCAAGG	840
187	CAGAGGCCTG	GGCTGGGAAA	AACTTTGGAA	CCAGACTCTT	GCCTGTTTCC	CAGGCCCACT	900
188	GTGCCTCAGA	GACCAGGGCT	CCAGCCCCTC	TTGGAGAAGT	CTCAGCTAAG	CTCACGTCCT	960
189	GAGAAAGCTC	AAAGGTTTGG	AAGGAGCAGA	AAACCCTTGG	GCCAGAAGTA	CCAGACTAGA	1020
190	TGGACCTGCC	TGCATAGGAG	TTTGGAGGAA	GTTGGAGTTT	TGTTTCCTCT	GTTCAAAGCT	1080
191	GCCTGTCCCT	ACCCCATGGT	GCTAGGAAGA	GGAGTGGGGT	GGTGTGAGAC	CCTGGAGGCC	1140
192	CCAACCCTGT	CCTCCCGAGC	TCCTCTTCCA	TGCTGTGCGC	CCAGGGCTGG	GAGGAAGGAC	1200
193	TTCCCTGTGT	AGTTTGTGCT	GTAAGAGATT	GCTTTTGTGT	TATTTAATGC	TGTGGCATGG	1260
194	GTGAAGAGGA	GGGGAAGAGG	CCTGTTTGGC	CTCTCTATCC	TCTCTTCCTC	TTCCCCCAAG	1320
195	ATTGAGCTCT	CTGCCCTTGA	TCAGCCCCAC	CCTGGCCTAG	ACCAGCAGAC	AGAGCCAGGA	1380
196	GAAGCTCAGC	TGCATTCCGC	AGCCCCCACC	CCCAAGGTTC	TCCAACATCA	CAGCCCAGCC	1440
197	CGCCCCTGCG	GTAATAAAAG	TGGTTTGTGG	AAAAAAAAAA	AAAAAAAAAA	AAGTCCTGCG	1500
198	GCCGC						1505

200 (2) INFORMATION FOR SEQ ID NO: 5:

201 (i) SEQUENCE CHARACTERISTICS:

202 (A) LENGTH: 2002 base pairs

203 (B) TYPE: nucleic acid

204 (C) STRANDEDNESS: single

205 (D) TOPOLOGY: linear

206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

208	GAATTCGGCA	CGAGGGCCAT	GGCCGGGCTA	TCCCGCGGGT	CCGCGCGCGC	ACTGCTCGCC	60
209	GCCCTGCTGG	CGTCGACGCT	GTTGGCGCTG	CTCGTGTCGC	CCGCGCGGGG	TCGCGGCGGC	120
210	CGGGACCACG	GGGACTGGGA	CGAGGCCTCC	CGGCTGCCGC	CGCTACCACC	CCGCGAGGAC	180
211	GCGGCGCGCG	TGGCCCGCTT	CGTGACGCAC	GTCTCCGACT	GGGGCGCTCT	GGCCACCATC	240
212	TCCACGCTGG	AGGCGGTGCG	CGGCCGGCCC	TTCCCGCAGC	TCCTCTCGCT	CAGCGACGGG	300
213	CCCCCGGGCG	CGGGCAGCGG	CGTGCCCTAT	TTCTACCTGA	GCCCGCTGCA	GCTCTCCGTG	360
214	AGCAACCTGC	AGGAGAATCC	ATATGCTACA	CTGACCATGA	CTTTGGCACA	GACCAACTTC	420
215	TGCAAGAAAC	ATGGATTTGA	TCCACAAAGT	CCCCTTTGTG	TTACATAAAT	GCTGTCAGGA	480
216	ACTGTGACCA	AGGTGAATGA	AACAGAAATG	GATATTGCAA	AGCATTCGTT	ATTCATTCTGA	540



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217 CACCCTGAGA TGAAAACCTG GCCTTCCAGC CATAATTGGT TCTTTGCTAA GTTGAATATA 600
218 ACCAATATCT GGGTCCTGGA CTACTTTGGT GGACCAAAAA TCGTGACACC AGAAGAATAT 660
219 TATAATGTCA CAGTTCAGTG AAGCAGACTG TGGTGAATTT AGCAACACTT ATGAAGTTTC 720
220 TTAAAGTGGC TCATACACAC TTAAAAGGCT TAATGTTTCT CTGGAAAGCG TCCCAGAATA 780
221 TTAGCCAGTT TTCTGTCACA TGCTGGTTTG TTTGCTTGCT TGTTTACTTG CTTGTTTACC 840
222 AATAGAGTTG ACCTGTTATT GGATTTCTCT GAAGATGTGG TAGCTACTTT TTTCTATTT 900
223 TGAAGCCATT TTCGTAGAGA AATATCCTTC ACTATAATCA AATAAGTTTT GTCCCATCAA 960
224 TTCCAAAGAT GTTTCAGTG GTGCTCTTGA AGAGGAATGA GTACCAGTTT TAAATTGCCC 1020
225 ATTGGCATTG GAAGGTAGTT GAGTATGTGT TCTTTATTCC TAGAAGCCAC TGTGCTTGGT 1080
226 AGAGTGCATC ACTCACCACA GCTGCCTCTT GAGCTGCCTG AGCCTGGTGC AAAAGGATTG 1140
227 GCCCCATTA TGGTGCTTCT GAATAAATCT TGCCAAGATA GACAAACAAT GATGAAACTC 1200
228 AGATGGAGCT TCCTACTCAT GTTGATTTAT GTCTCACAAT CCTGGGTATT GTTAATTCAA 1260
229 CATAGGGTGA AACTATTTCT GATAAAGAAC TTTTGAAAAA CTTTTTATAC TCTAAAGTGA 1320
230 TACTCAGAAC AAAAGAAAGT CATAAACTC CTGAATTTAA TTTCCCCACC TAAGTCGAGA 1380
231 CAGTATTATC AAAACACATG TGCACACAGA TTATTTTTTG GCTCCAAAAC TGGATTGCAA 1440
232 AAGAAAGAGG AGAGATATTT TGTGTGTTCC TGGTATTCTT TTATAAGTAA AGTTACCCAG 1500
233 GCATGGACCA GCTTCAGCCA GGGACAAAAT CCCCTCCCAA ACCACTCTCC ACAGCTTTTT 1560
234 AAAAATACTT CTA CTCTTAA CAATTACCTA AGGTCCTTC AAACCCCCC AACTCTTAAT 1620
235 AGCTTCTAGT GCTGCTACAA TCTAAGTCAG GTCACCAGAG GGAAGAGAAC ATGGCATTAA 1680
236 AAGAATCACA TCTTCAGAAG AGAAGACACT AATATTATTA CCCATATACA TGATTTTCAA 1740
237 AGATGACATA AGATTCCTCT TAAAGAGGAA ATGTCAGGAA TCAAGCCACT GAATCCTTAA 1800
238 AGAGAAAAGT TGAATATGAG TCATTGTGTC TGAAAACCTG AAAGTGAAC TAACTGAGAT 1860
239 CCAGCAAACA GGTCTGTGTT AAGAAAAATA ATTTATACTA AATTTAGTAA AATGGACTTC 1920
240 TTATTCAAAG CATCAATAAT TAAAAGAATT ATTTTAAAAA AAAAAAAAAA AAAAAAAAAA 1980
241 AAAAAAAAAA TCCTGCGGCC GC 2002
243 (2) INFORMATION FOR SEQ ID NO: 6:
244 (i) SEQUENCE CHARACTERISTICS:
245 (A) LENGTH: 1322 base pairs
246 (B) TYPE: nucleic acid
247 (C) STRANDEDNESS: single
248 (D) TOPOLOGY: linear
249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
251 GAATTCGGCA CGAGGGCCAC GACTCTGCTG GCATTTCTTC TATAGCCACT GGAATCTGAT 60
252 CCTGATTGTC TTCCACTACT ACCAGGCCAT CACCACTCCG CCTGGGTACC CACCCCAGGG 120
253 CAGGAATGAT ATCGCCACCG TCTCCATCTG TAAGAAGTGC ATTTACCCCA AGCCAGCCCG 180
254 AACACACCAC TGCAGCATCT GCAACAGGTG TGTGCTGAAG ATGGATCACC ACTGCCCTG 240
255 GCTAAACAAT TGTGTGGGCC ACTATAACCA TCGGTACTTC TTCTCTTTCT GCTTTTTTCAT 300
256 GACTCTGGGC TGTGTCTACT GCAGCTATGG AAGTTGGGAC CTTTTCCGGG AGGCTTATGC 360
257 TGCCATTGAG AAAATGAAAC AGCTCGACAA GAACAAACTA CAGGCGGTTG CCAACCAGAC 420
258 TTATCACCAG ACCCCACCAC CCACCTTCTC CTTTCGAGAA AGGATGACTC ACAAGAGTCT 480
259 TGTCTACCTC TGGTTCCTGT GCAGTTCTGT GGCATTGCC CTGGGTGCC TAACTGTATG 540
260 GCATGCTGTT CTCATCAGTC GAGGTGAGAC TAGCATCGAA AGGCACATCA ACAAGAAGGA 600
261 GAGACGTCGG CTACAGGCCA AGGGCAGAGT ATTTAGGAAT CCTTACAAC ACGGCTGCTT 660
262 GGACAACTGG AAGGTATTCC TGGGTGTGGA TACAGGAAGG CACTGGCTTA CTCGGGTGCT 720
263 CTTACCTTCT ACTCACTTGC CCCATGGGAA TGGAATGAGC TGGGAGCCCC CTCCCTGGGT 780
264 GACTGCTCAC TCAGCCTCTG TGATGGCAGT GTGAGCTGGA CTGTGTCAGC CACGACTCGA 840
265 GCACTCATTC TGCTCCCTAT GTTATTTCAA GGGCCTCCAA GGGCAGCTTT TCTCAGAATC 900
266 CTTGATCAAA AAGAGCCAGT GGGCCTGCCT TAGGGTACCA TGCAGGACAA TTCAAGGACC 960
267 AGCCTTTTAA CCACTGCAGA AGAAAGACAC AATGTGGAGA AATCTTAGGA CTGACATCCC 1020

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/935,390A

DATE: 11/19/2001

TIME: 15:40:34

Input Set : N:\Crf3\RULE60\09935390A.txt

Output Set: N:\CRF3\11192001\I935390A.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:56 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1  
L:714 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20  
L:798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21  
L:864 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22  
L:931 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23  
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24  
L:1032 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25  
L:1081 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26  
L:1179 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27  
L:1237 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28  
L:1289 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29  
L:1350 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30  
L:1408 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31  
L:1490 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32  
L:1548 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33  
L:1630 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34  
L:1704 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35  
L:1768 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36  
L:1820 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37  
L:1920 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38